

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/538,038A
Source: IFwo
Date Processed by STIC: 6/20/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/10/06

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>10/538,038A</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input checked="" type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules , each n or Xaa can only represent a single residue . Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/538,038A

DATE: 06/20/2006
TIME: 15:28:31

Input Set : A:\Sequence Listing.TXT
Output Set: N:\CRF4\06202006\J538038A.raw

2 <110> APPLICANT: Givaudan SA
W--> 3 <120> TITLE OF INVENTION: G-Proteins
W--> 4 <130> FILE REFERENCE: 30069PCT
W--> 5 <140> CURRENT APPLICATION NUMBER: US 10/538,038A
C--> 6 <141> CURRENT FILING DATE: 2005-06-08
7 <150> PRIOR APPLICATION NUMBER: US 60/434,790
8 <151> PRIOR FILING DATE: 2002-12-18
W--> 9 <160> NUMBER OF SEQ ID: 2

ERRORED SEQUENCES

W--> 10 <210> SEQ ID NO: 1
11 <211> LENGTH: 1122 <212> DNA
12 <213> ORGANISM: Homo sapiens
W--> 13 <220> FEATURE:
14 <221> NAME/KEY: CDS
15 <222> LOCATION: (1)..(1122)
16 <223> OTHER INFORMATION:
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W--> 17 <400> SEQUENCE: 1

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20 ggggagctga	agctgctgct	tttggggcca	ggcgagagcg	ggaagagcac	tttcatcaag	180
21 cagatgcgga	tcatccacgg	cggccgctac	tcggaggagg	agcgaagagg	cttcggccc	240
22 ctggtctacc	agaacatctt	cgtgtccatg	cgggccatga	tcgaggccat	ggagcggctg	300
23 cagattccat	tcagcaggcc	cgagagcaag	caccacgcta	gcctggtcat	gagccaggac	360
24 ccctataaag	tgaccacgtt	tgagaagcgc	tacgctgcgg	ccatgcagtg	gctgtggagg	420
25 gatgccggca	tccgggcctg	ctatgagcgt	cggcggaaat	tccacctgct	cgattcagcc	480
26 gtgtactacc	tgtcccacct	ggagcgcatac	accgaggagg	gctacgtccc	cacagctcag	540
27 gacgtgctcc	gcagcccat	gccaccact	ggcatcaacg	agtaactgctt	ctccgtgcag	600
28 aaaaccaacc	tgcggatcgt	ggacgtcggg	ggccagaagt	cagacgtaa	gaaatggatc	660
29 cattgtttcg	agaacgtgat	cggcctcatac	tacctggct	cactgagtga	atacgaccag	720
30 tgctctggagg	agaacaacca	ggagaaccgc	atgaaggaga	gcctcgatt	gttggact	780
31 atcctggAAC	taccctggTT	caaaAGcaca	tccgtcatcc	tcttctcaa	caaaACCGAC	840
32 atcctggagg	agaaaATCCC	cacctcccac	ctggctacct	atttccccag	tttccaggc	900
33 cctaaggcagg	atgctgaggc	agccaagagg	ttcattctgg	acatgtacac	gaggatgtac	960
34 accgggtgcg	tggacggccc	cgagggcagc	aactaaaaaa	aagaagataa	ggaatctat	1020
35 tctcacatga	cctgcgtac	tgacacacaa	aacgtcaaAT	tcgtgtttga	tgccgtgaca	1080
36 gatataataa	taaaagagaa	cctcaaagac	tgtggctct	tc		1122

38 <210> SEQ ID NO: 2

39 <211> LENGTH: 374

40 <212> TYPE: PRT

Does Not Comply
Corrected Diskette Needed

insert a hard return

See
ppr 1-3

? (see p.3 - the last-numbered arrow and
states "395")

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/538,038A

DATE: 06/20/2006

TIME: 15:28:31

Input Set : A:\Sequence Listing.TXT

Output Set: N:\CRF4\06202006\J538038A.raw

41 <213> ORGANISM: Homo sapiens

W--> 42 <400> SEQUENCE: 2

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2215 2220 2225 2230 2235 2240 2245 2250 2255 2260 2265 2270 2275 2280 2285 2290 2295 2300 2305 2310 2315 2320 2325 2330 2335 2340 2345 2350 2355 2360 2365 2370 2375 2380 2385 2390 2395 2400 2405 2410 2415 2420 2425 2430 2435 2440 2445 2450 2455 2460 2465 2470 2475 2480 2485 2490 2495 2500 2505 2510 2515 2520 2525 2530 2535 2540 2545 2550 2555 2560 2565 2570 2575 2580 2585 2590 2595 2600 2605 2610 2615 2620 2625 2630 2635 2640 2645 2650 2655 2660 2665 2670 2675 2680 2685 2690 2695 2700 2705 2710 2715 2720 2725 2730 2735 2740 2745 2750 2755 2760 2765 2770 2775 2780 2785 2790 2795 2800 2805 2810 2815 2820 2825 2830 2835 2840 2845 2850 2855 2860 2865 2870 2875 2880 2885 2890 2895 2900 2905 2910 2915 2920 2925 2930 2935 2940 2945 2950 2955 2960 2965 2970 2975 2980 2985 2990 2995 3000 3005 3010 3015 3020 3025 3030 3035 3040 3045 3050 3055 3060 3065 3070 3075 3080 3085 3090 3095 3100 3105 3110 3115 3120 3125 3130 3135 3140 3145 3150 3155 3160 3165 3170 3175 3180 3185 3190 3195 3200 3205 3210 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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/538,038A

DATE: 06/20/2006
TIME: 15:28:31

Input Set : A:\Sequence Listing.TXT
Output Set: N:\CRF4\06202006\J538038A.raw

E--> 114 370
E--> 116 Phe Gln Gly Pro Lys Gin Asp
E--> 117 385 390

375

380

invalid amino acid designator

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/538,038A

DATE: 06/20/2006

TIME: 15:28:32

Input Set : A:\Sequence Listing.TXT

Output Set: N:\CRF4\06202006\J538038A.raw

L:3 M:283 W: Missing Blank Line separator, <120> field identifier
L:4 M:283 W: Missing Blank Line separator, <130> field identifier
L:5 M:283 W: Missing Blank Line separator, <140> field identifier
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:9 M:283 W: Missing Blank Line separator, <160> field identifier
L:10 M:283 W: Missing Blank Line separator, <210> field identifier
L:13 M:283 W: Missing Blank Line separator, <220> field identifier
L:17 M:282 E: Numeric Field Identifier Missing, <212> is required.
L:17 M:283 W: Missing Blank Line separator, <400> field identifier
L:17 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:16
L:42 M:283 W: Missing Blank Line separator, <400> field identifier
L:44 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:98 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:116 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1